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Docket No.: 524412000200
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:

    Lee A. BULLA, Jr. et al.

Application No.: 09/696,801

Filed: October 25, 2000

For: GENE MINING SYSTEM AND METHOD

Confirmation # 3203

Art Unit: 1631

Examiner: Lori A. Clow, Ph.D.

AMENDMENT UNDER 37 C.F.R. § 1.312(a)

MS Issue Fee
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

It has been brought to the attention of the undersigned that no sequence listing in compliance

with 37 C.F.R. §§ 1.821, *et seq.*, has been submitted in this application. The application as filed

refers to eight nucleotide or amino acid sequences. As none of these sequences are germane to the

claims as allowed, the present amendment proposes to cancel radio frequencies to these sequences,

thus making submission of a sequence listing unnecessary. Thus, applicants propose to amend the

specification as set forth below.

sd-245645

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AMENDMENT

On page 11, please delete the paragraph at lines 3-4:

"Figure 14 is ... the present invention."

Please delete the section beginning on page 12, at line 22, and continuing to page 14, line 14:

"The invention thus includes nucleic acid ... CDS III/3' TRUN)."

On pages 59-60, please amend the bridging paragraph as follows:

Following the initial identification of a target and the filtering of sequences, an alignment of the beta integrin proteins that were identified from all organisms was conducted and primer selection was made based on the identified matching sequences between the different organisms. The primer design software was the MacVector software, and following an initial round of sequence determination, the primer design was improved. ~~The exact primers used are provided in the SEQ ID Listing.~~

On page 60, please amend the paragraph at lines 11-17 as follows:

The insert from these clones was then used to clone the full-length cDNA from a *M. sexta* library. ~~The sequence of integrin beta 1 (ITGB1) gene is depicted in FIGURE 14 as SEQ ID NO.:1 and the corresponding amino acid sequence is at SEQ ID NO.: 2. These sequences represent preliminary sequence data, and the sequences will be completed and confirmed by methods known in the art.~~

On pages 60-61, please delete the bridging paragraph:

"The closest homology of ... the entire sequence of the novel gene."

Please delete Figure 14.

sd-245645   2